FIG. 1

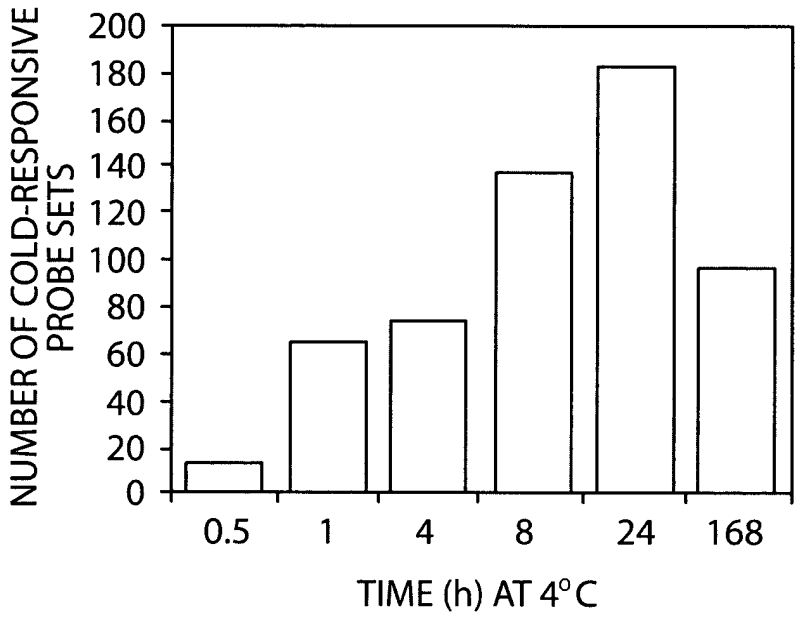

NUMBER OF COLD-RESPONSIVE PROBE SETS
200
180
160
140
120
100
80
60
40
20
0
0.5
1
4
8
24
168
TIME (h) AT 4°C

FIG. 2

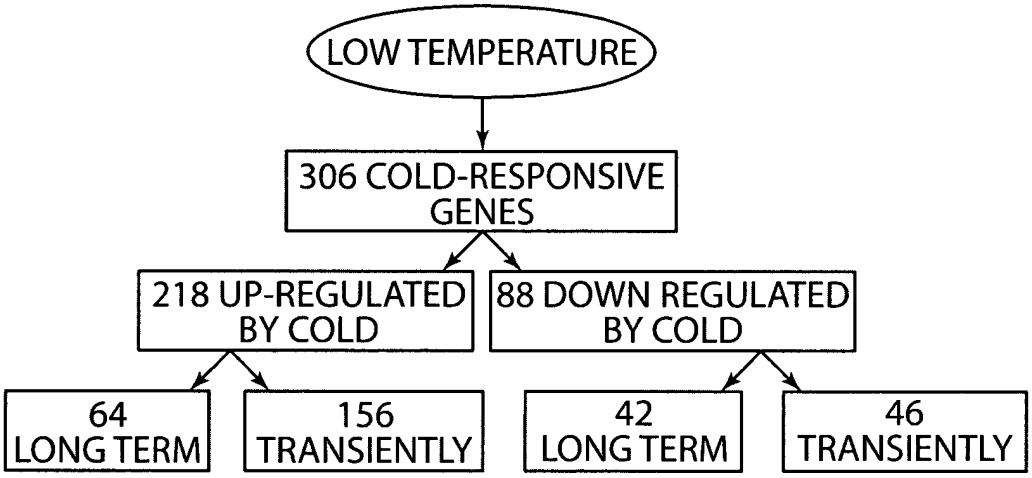

LOW TEMPERATURE
306 COLD-RESPONSIVE GENES
218 UP-REGULATED BY COLD
88 DOWN REGULATED BY COLD
64 LONG TERM
156 TRANSIENTLY
42 LONG TERM
46 TRANSIENTLY

FIG. 3

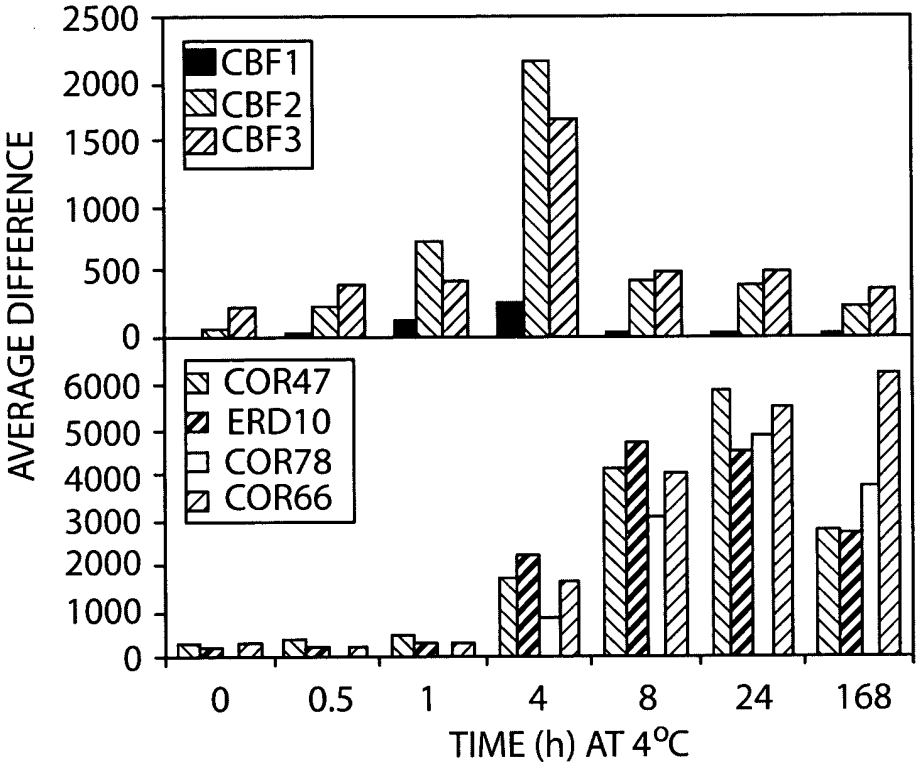

AVERAGE DIFFERENCE
2500
2000
1500
1000
500
0
CBF1
CBF2
CBF3
6000
5000
4000
3000
2000
1000
0
COR47
ERD10
COR78
COR66
0
0.5
1
4
8
24
168
TIME (h) AT 4°C

FIG. 4A

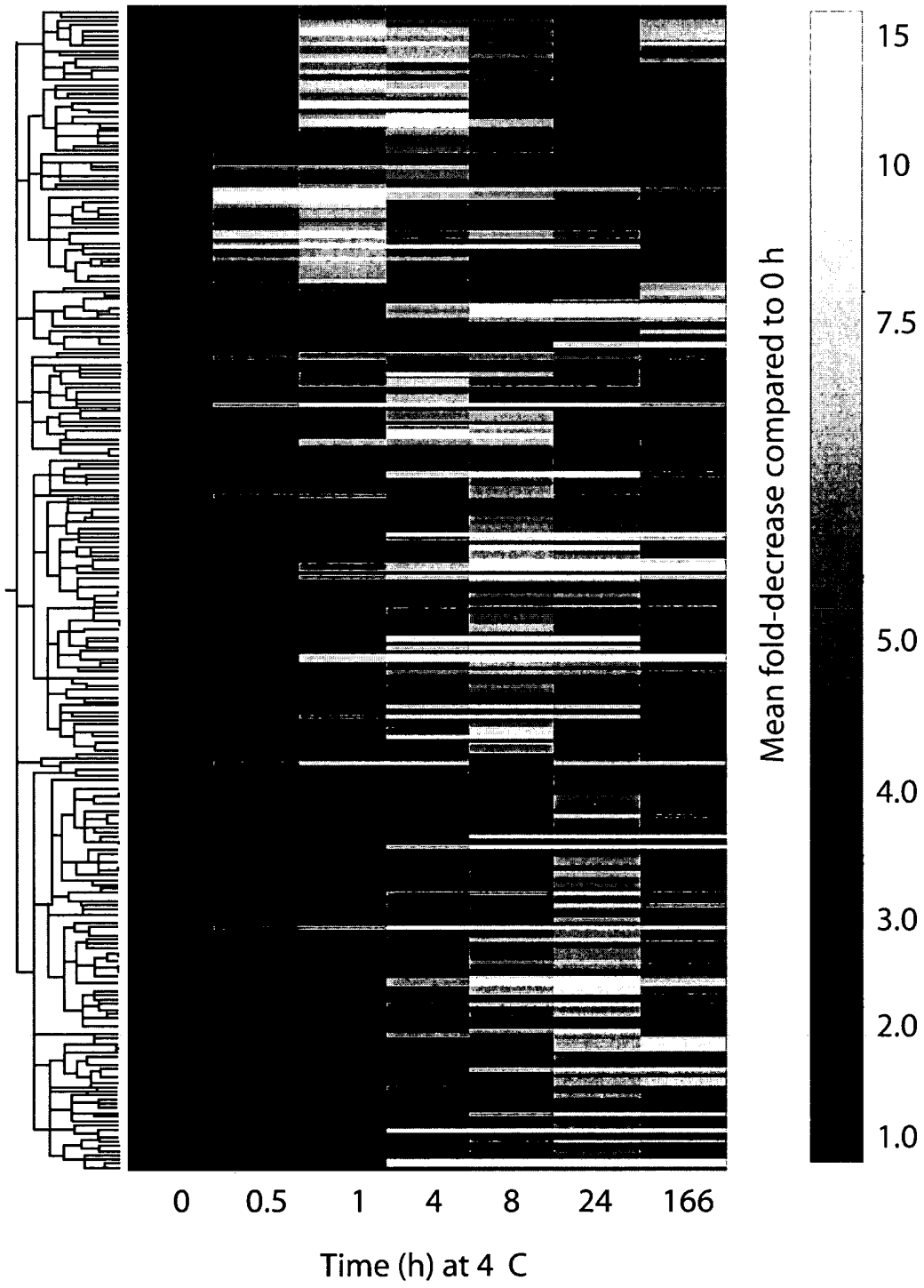

15
10
7.5
5.0
4.0
3.0
2.0
1.0
Mean fold-decrease compared to 0 h
0
0.5
1
4
8
24
166
Time (h) at 4 C

FIG. 4B

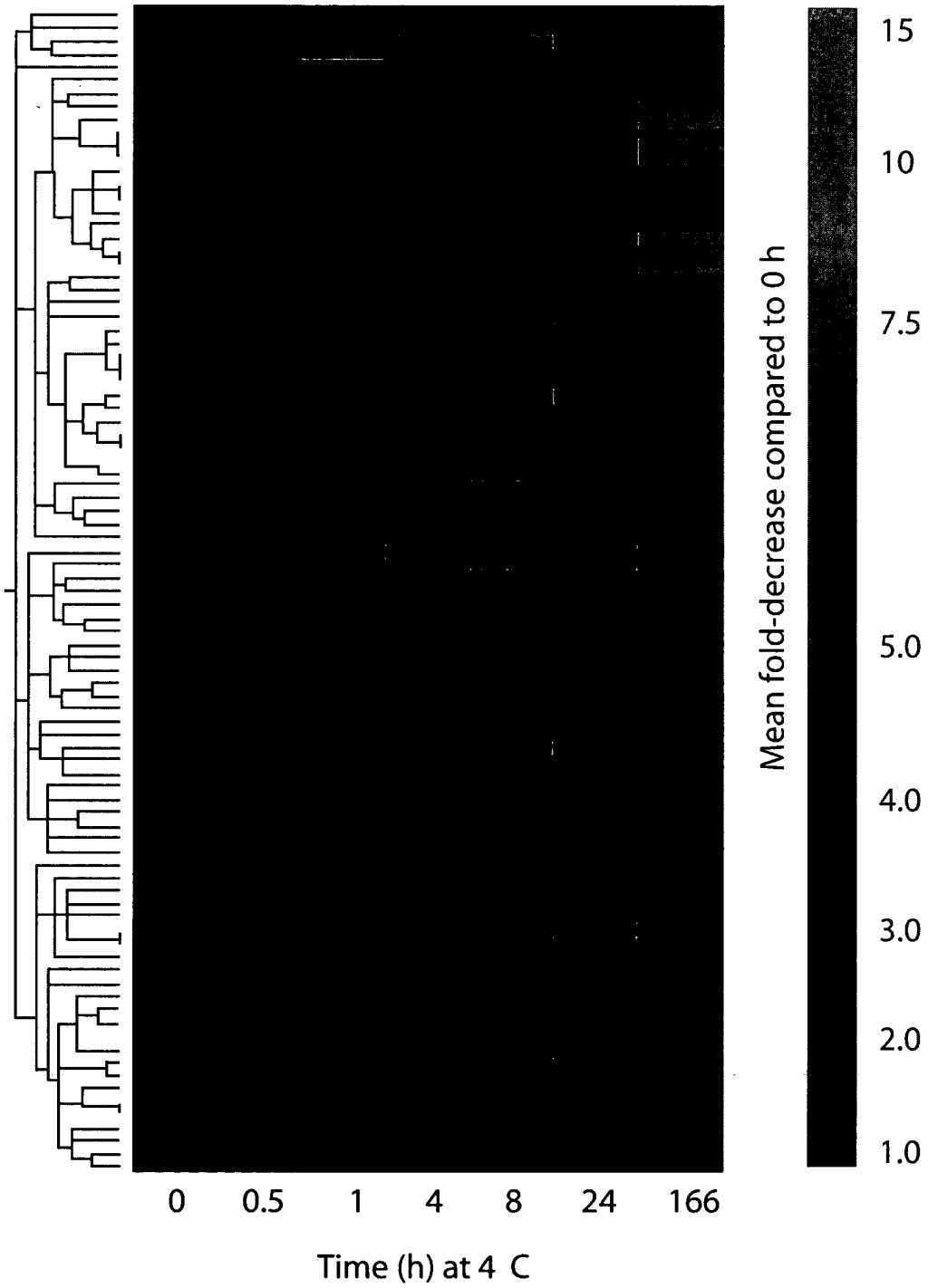

15
10
7.5
5.0
4.0
3.0
2.0
1.0
Mean fold-decrease compared to 0 h
0
0.5
1
4
8
24
166
Time (h) at 4 C

FIG. 5A

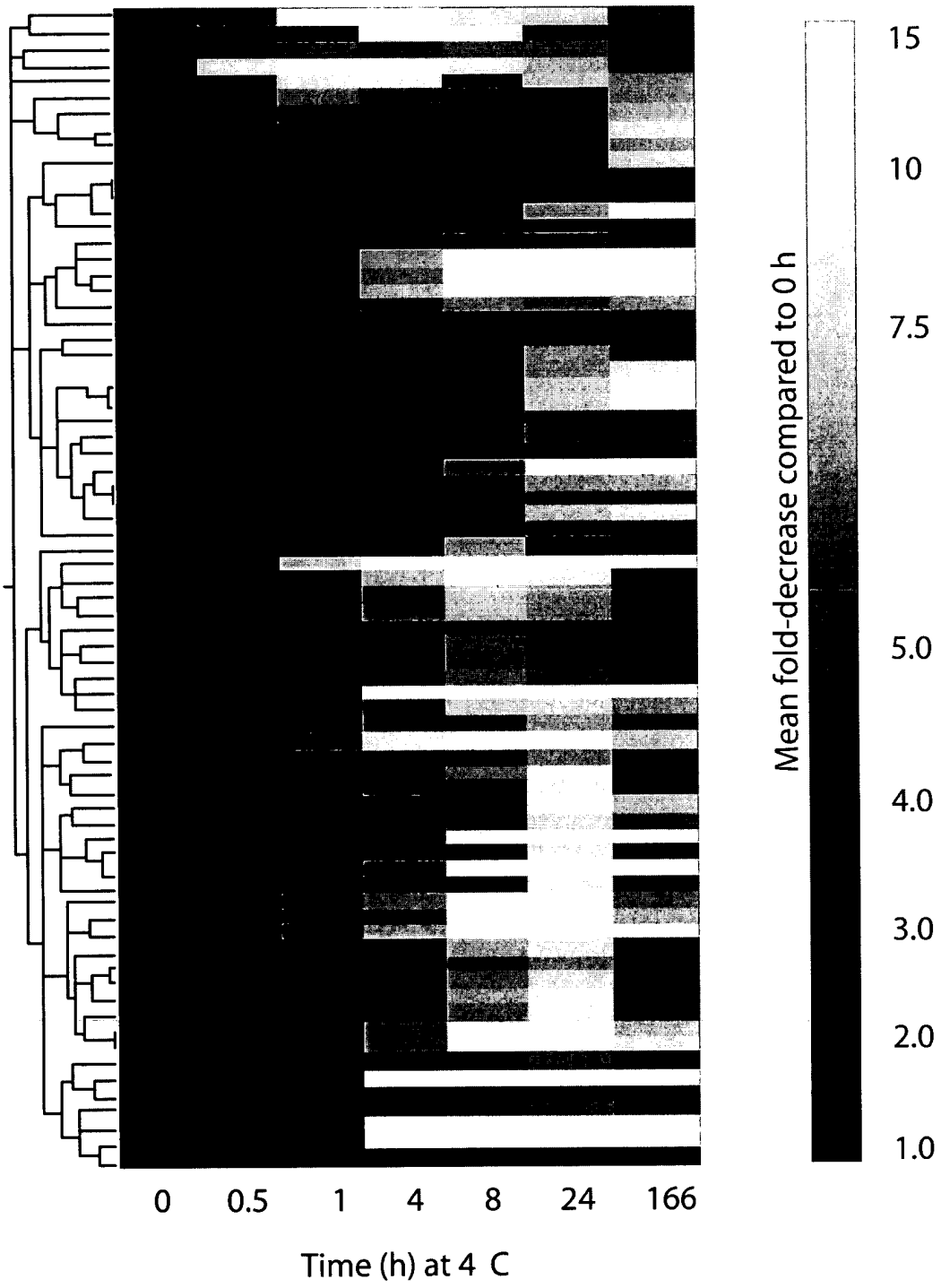

15
10
7.5
5.0
4.0
3.0
2.0
1.0
Mean fold-decrease compared to 0 h
0
0.5
1
4
8
24
166
Time (h) at 4 C

FIG. 5B

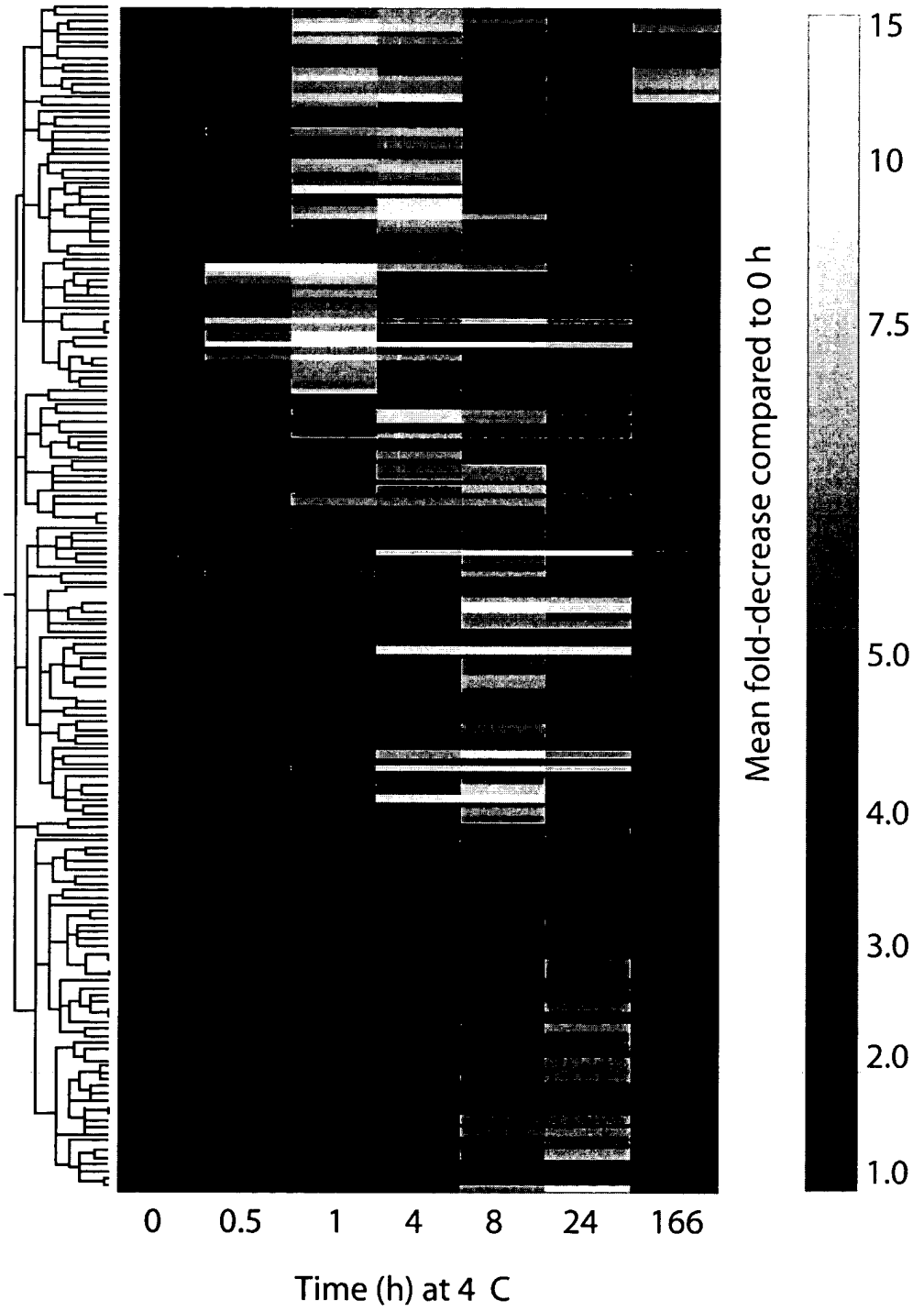

15
10
7.5
5.0
4.0
3.0
2.0
1.0
Mean fold-decrease compared to 0 h
0
0.5
1
4
8
24
166
Time (h) at 4 C

FIG. 6

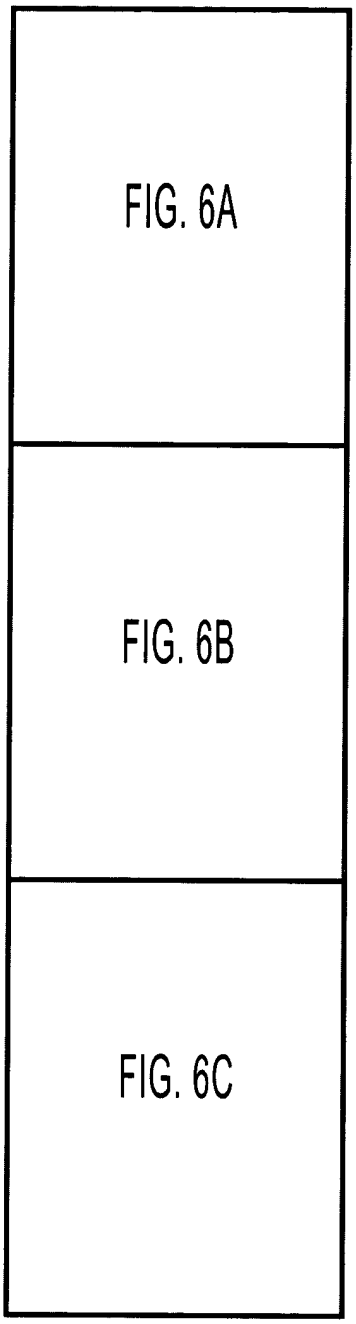


FIG. 6A

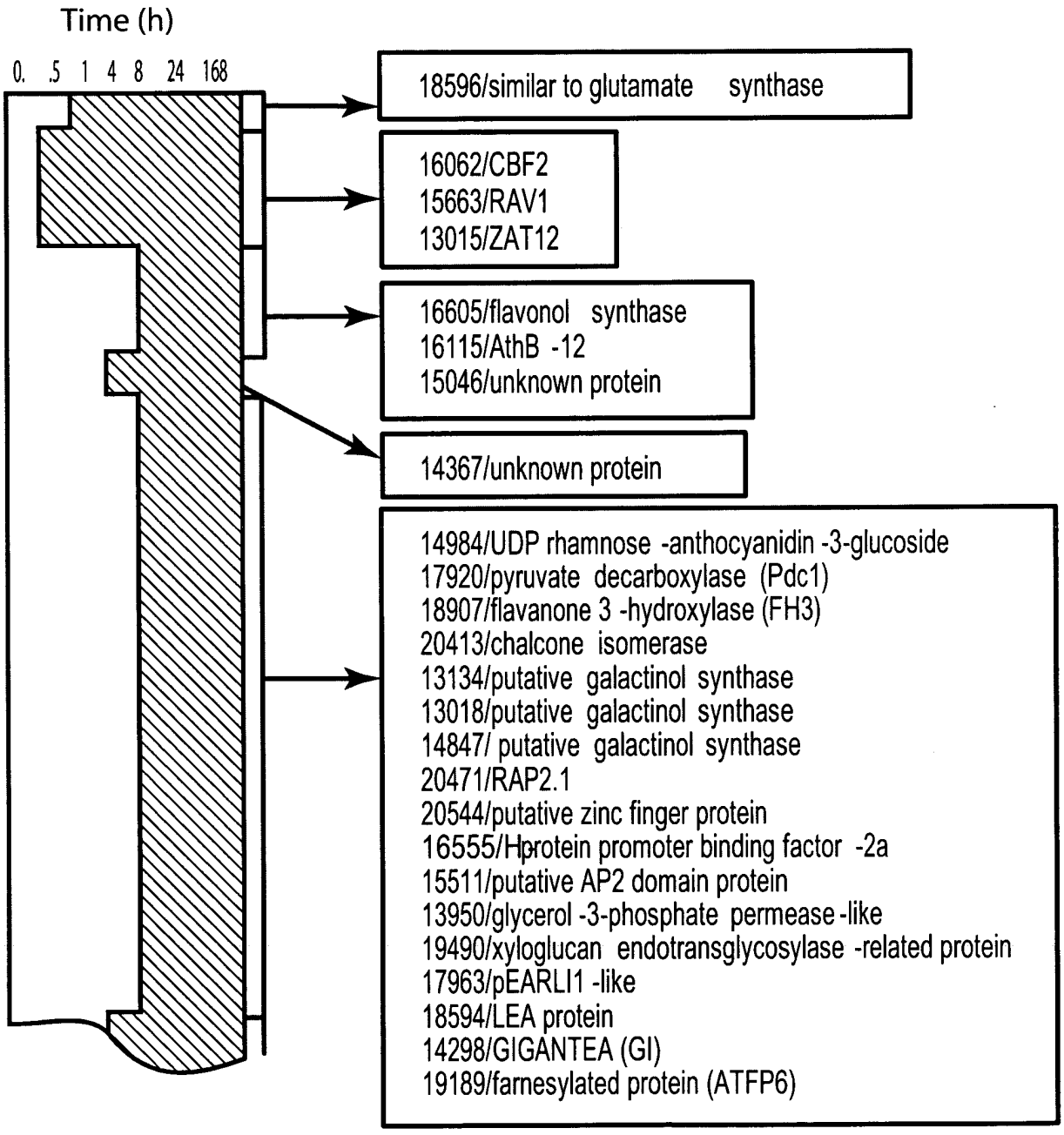

Time (h)
0. .5 1 4 8 24 168
18596/similar to glutamate synthase
16062/CBF2
15663/RAV1
13015/ZAT12
16605/flavonol synthase
16115/AthB -12
15046/unknown protein
14367/unknown protein
14984/UDP rhamnose -anthocyanidin -3-glucoside
17920/pyruvate decarboxylase (Pdc1)
18907/flavanone 3 -hydroxylase (FH3)
20413/chalcone isomerase
13134/putative galactinol synthase
13018/putative galactinol synthase
14847/ putative galactinol synthase
20471/RAP2.1
20544/putative zinc finger protein
16555/Hprotein promoter binding factor -2a
15511/putative AP2 domain protein
13950/glycerol -3-phosphate permease -like
19490/xyloglucan endotransglycosylase -related protein
17963/pEARLI1 -like
18594/LEA protein
14298/GIGANTEA (GI)
19189/farnesylated protein (ATFP6)

FIG. 6B

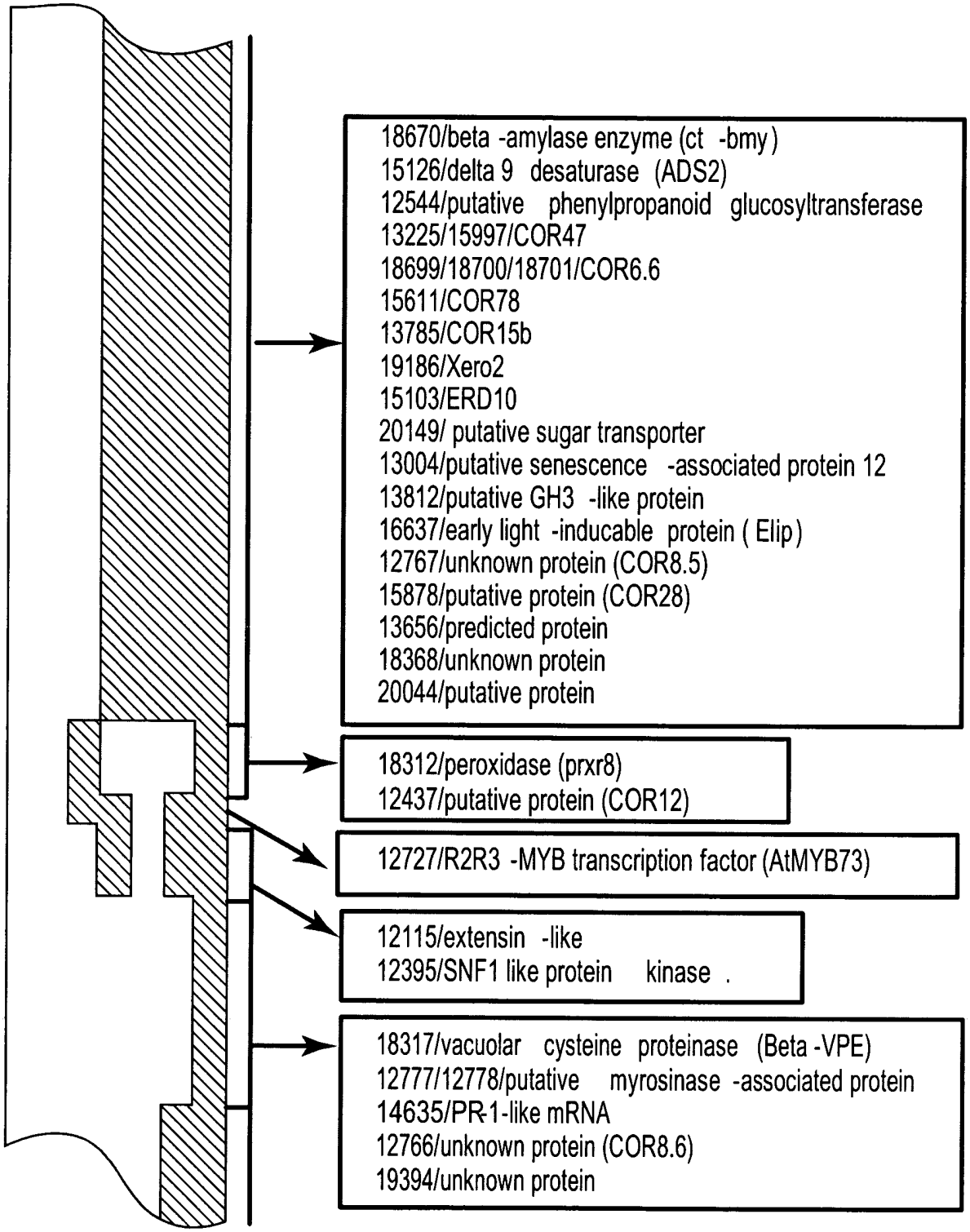

18670/beta -amylase enzyme (ct -bmy)
15126/delta 9 desaturase (ADS2)
12544/putative phenylpropanoid glucosyltransferase
13225/15997/COR47
18699/18700/18701/COR6.6
15611/COR78
13785/COR15b
19186/Xero2
15103/ERD10
20149/ putative sugar transporter
13004/putative senescence -associated protein 12
13812/putative GH3 -like protein
16637/early light -inducable protein (Elip)
12767/unknown protein (COR8.5)
15878/putative protein (COR28)
13656/predicted protein
18368/unknown protein
20044/putative protein
18312/peroxidase (prxr8)
12437/putative protein (COR12)
12727/R2R3 -MYB transcription factor (AtMYB73)
12115/extensin -like
12395/SNF1 like protein kinase .
18317/vacuolar cysteine proteinase (Beta -VPE)
12777/12778/putative myrosinase -associated protein
14635/PR-1-like mRNA
12766/unknown protein (COR8.6)
19394/unknown protein

FIG. 6C

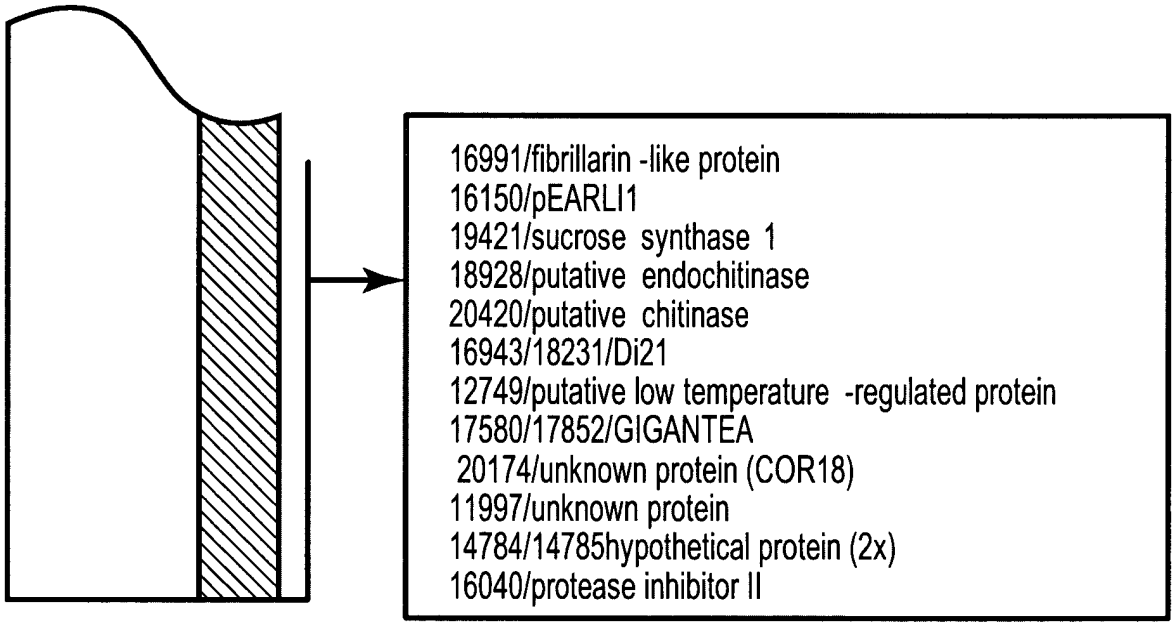

16991/fibrillarin -like protein
16150/pEARLI1
19421/sucrose synthase 1
18928/putative endochitinase
20420/putative chitinase
16943/18231/Di21
12749/putative low temperature -regulated protein
17580/17852/GIGANTEA
20174/unknown protein (COR18)
11997/unknown protein
14784/14785hypothetical protein (2x)
16040/protease inhibitor II

FIG. 7A

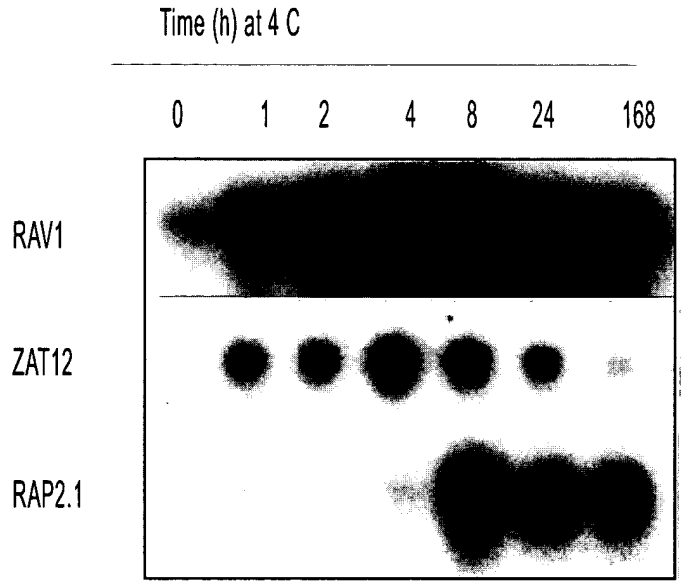

Time (h) at 4 C
0
1
2
4
8
24
168
RAV1
ZAT12
RAP2.1

FIG. 7B

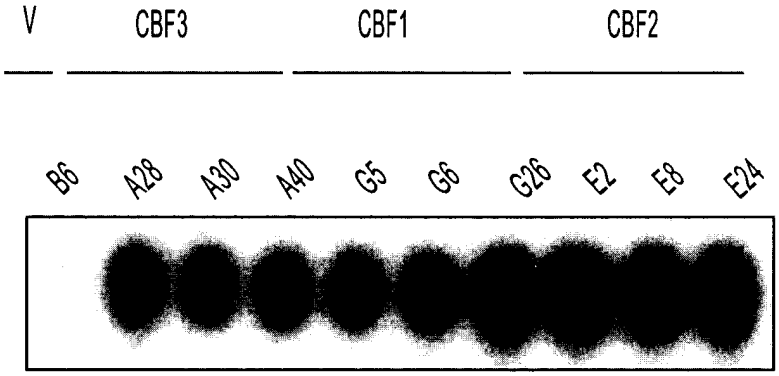

V
CBF3
CBF1
CBF2
B6
A28
A30
A40
G5
G6
G26
E2
E8
E24

FIG. 8

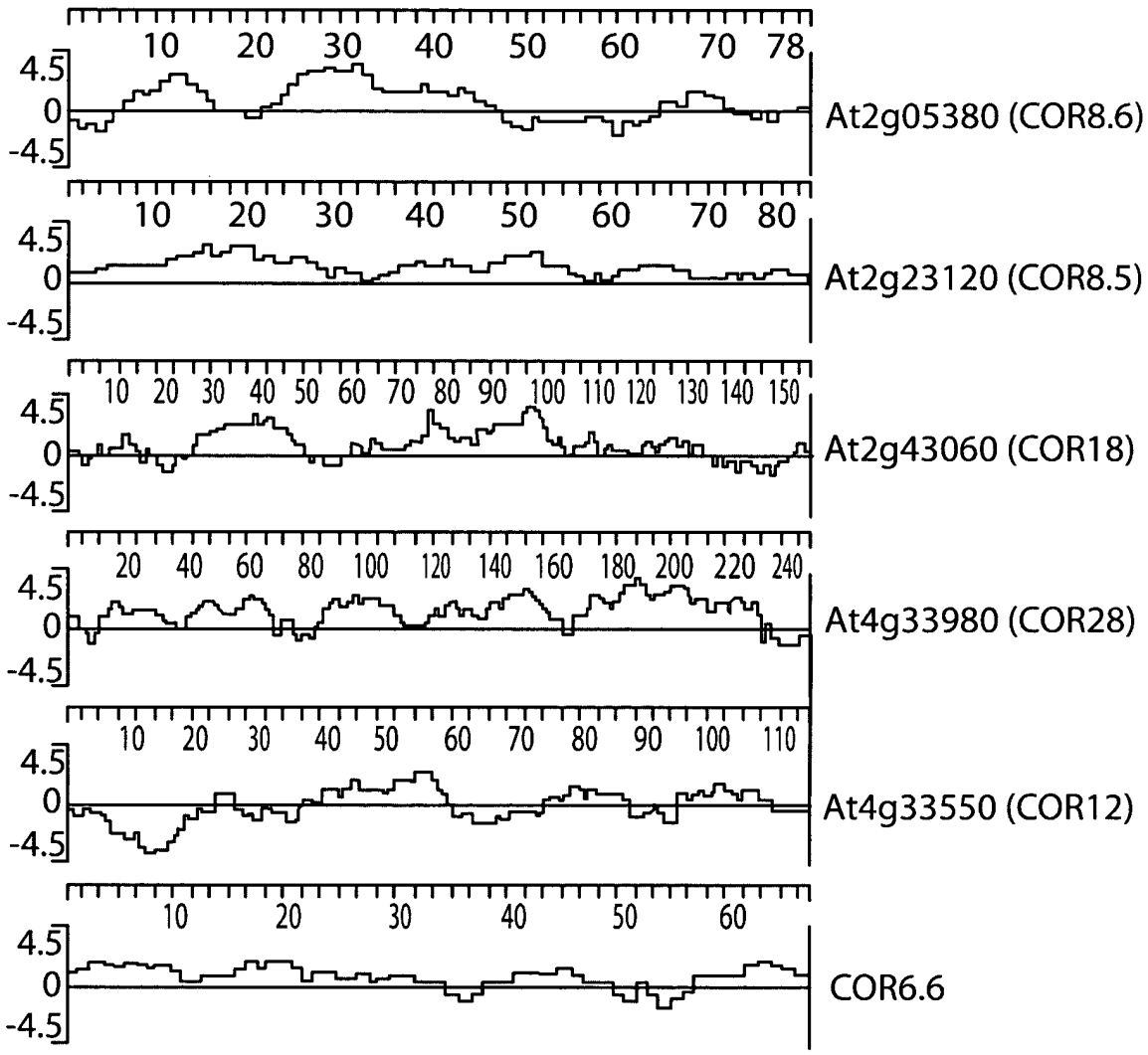
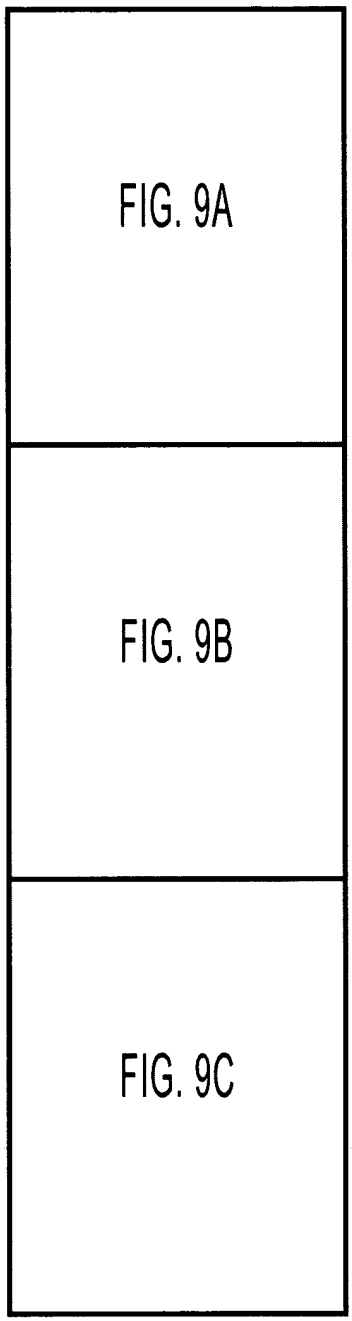

10 20 30 40 50 60 70 78
4.5
0
-4.5
At2g05380 (COR8.6)
10 20 30 40 50 60 70 80
4.5
0
-4.5
At2g23120 (COR8.5)
10 20 30 40 50 60 70 80 90 100 110 120 130 140 150
4.5
0
-4.5
At2g43060 (COR18)
20 40 60 80 100 120 140 160 180 200 220 240
4.5
0
-4.5
At4g33980 (COR28)
10 20 30 40 50 60 70 80 90 100 110
4.5
0
-4.5
At4g33550 (COR12)
10 20 30 40 50 60
4.5
0
-4.5
COR6.6

FIG. 9



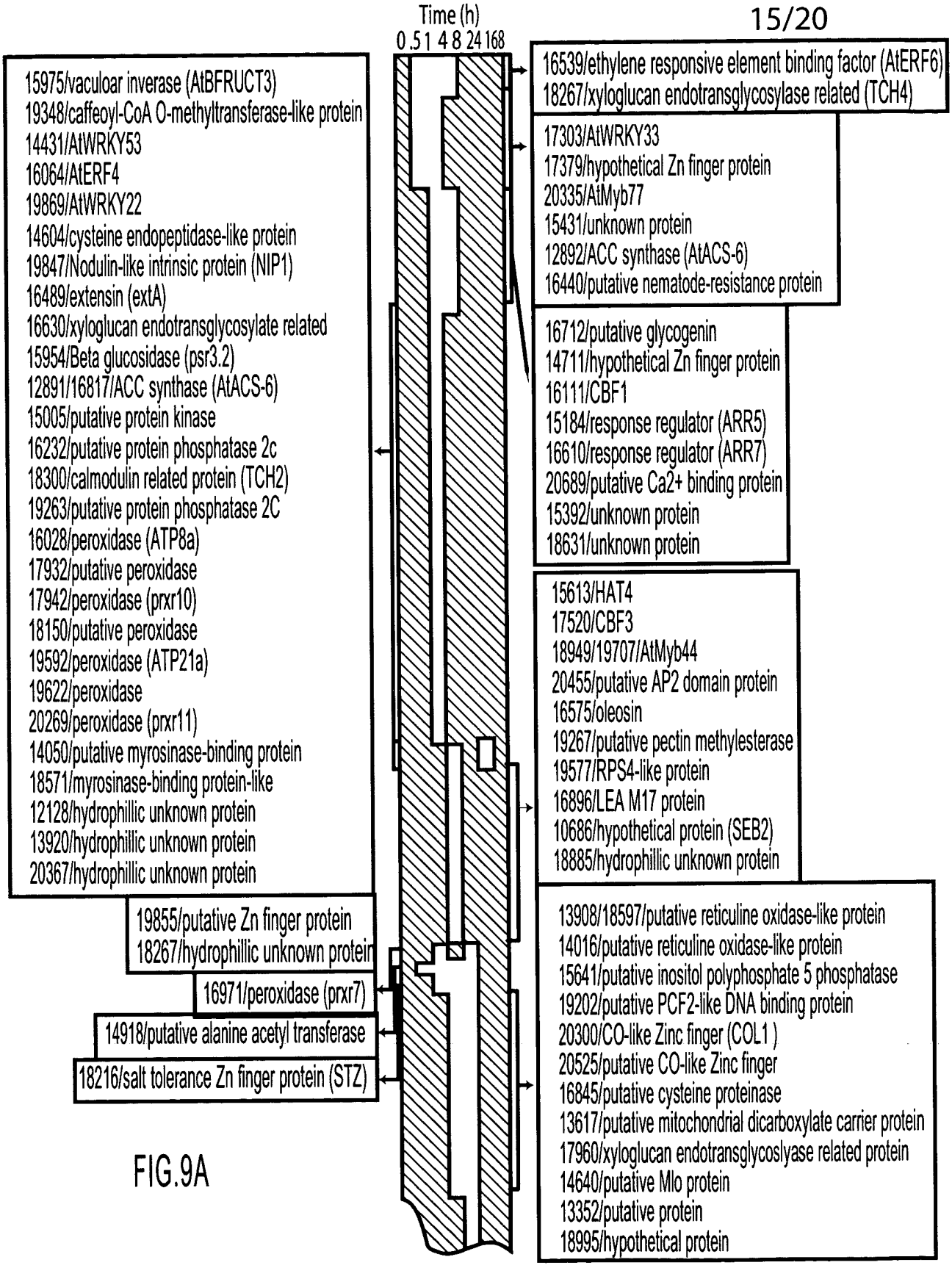

Time (h)
0 .5 1 4 8 24 168
15975/vaculoar inverase (AtBFRUCT3)
19348/caffeoyl-CoA O-methyltransferase-like protein
14431/AtWRKY53
16064/AtERF4
19869/AtWRKY22
14604/cysteine endopeptidase-like protein
19847/Nodulin-like intrinsic protein (NIP1)
16489/extensin (extA)
16630/xyloglucan endotransglycosylate related
15954/Beta glucosidase (psr3.2)
12891/16817/ACC synthase (AtACS-6)
15005/putative protein kinase
16232/putative protein phosphatase 2c
18300/calmodulin related protein (TCH2)
19263/putative protein phosphatase 2C
16028/peroxidase (ATP8a)
17932/putative peroxidase
17942/peroxidase (prxr10)
18150/putative peroxidase
19592/peroxidase (ATP21a)
19622/peroxidase
20269/peroxidase (prxr11)
14050/putative myrosinase-binding protein
18571/myrosinase-binding protein-like
12128/hydrophillic unknown protein
13920/hydrophillic unknown protein
20367/hydrophillic unknown protein
19855/putative Zn finger protein
18267/hydrophillic unknown protein
16971/peroxidase (prxr7)
14918/putative alanine acetyl transferase
18216/salt tolerance Zn finger protein (STZ)
16539/ethylene responsive element binding factor (AtERF6)
18267/xyloglucan endotransglycosylase related (TCH4)
17303/AtWRKY33
17379/hypothetical Zn finger protein
20335/AtMyb77
15431/unknown protein
12892/ACC synthase (AtACS-6)
16440/putative nematode-resistance protein
16712/putative glycogenin
14711/hypothetical Zn finger protein
16111/CBF1
15184/response regulator (ARR5)
16610/response regulator (ARR7)
20689/putative Ca2+ binding protein
15392/unknown protein
18631/unknown protein
15613/HAT4
17520/CBF3
18949/19707/AtMyb44
20455/putative AP2 domain protein
16575/oleosin
19267/putative pectin methylesterase
19577/RPS4-like protein
16896/LEA M17 protein
10686/hypothetical protein (SEB2)
18885/hydrophillic unknown protein
13908/18597/putative reticuline oxidase-like protein
14016/putative reticuline oxidase-like protein
15641/putative inositol polyphosphate 5 phosphatase
19202/putative PCF2-like DNA binding protein
20300/CO-like Zinc finger (COL1)
20525/putative CO-like Zinc finger
16845/putative cysteine proteinase
13617/putative mitochondrial dicarboxylate carrier protein
17960/xyloglucan endotransglycoslyase related protein
14640/putative Mlo protein
13352/putative protein
18995/hypothetical protein

FIG.9A

FIG. 9B

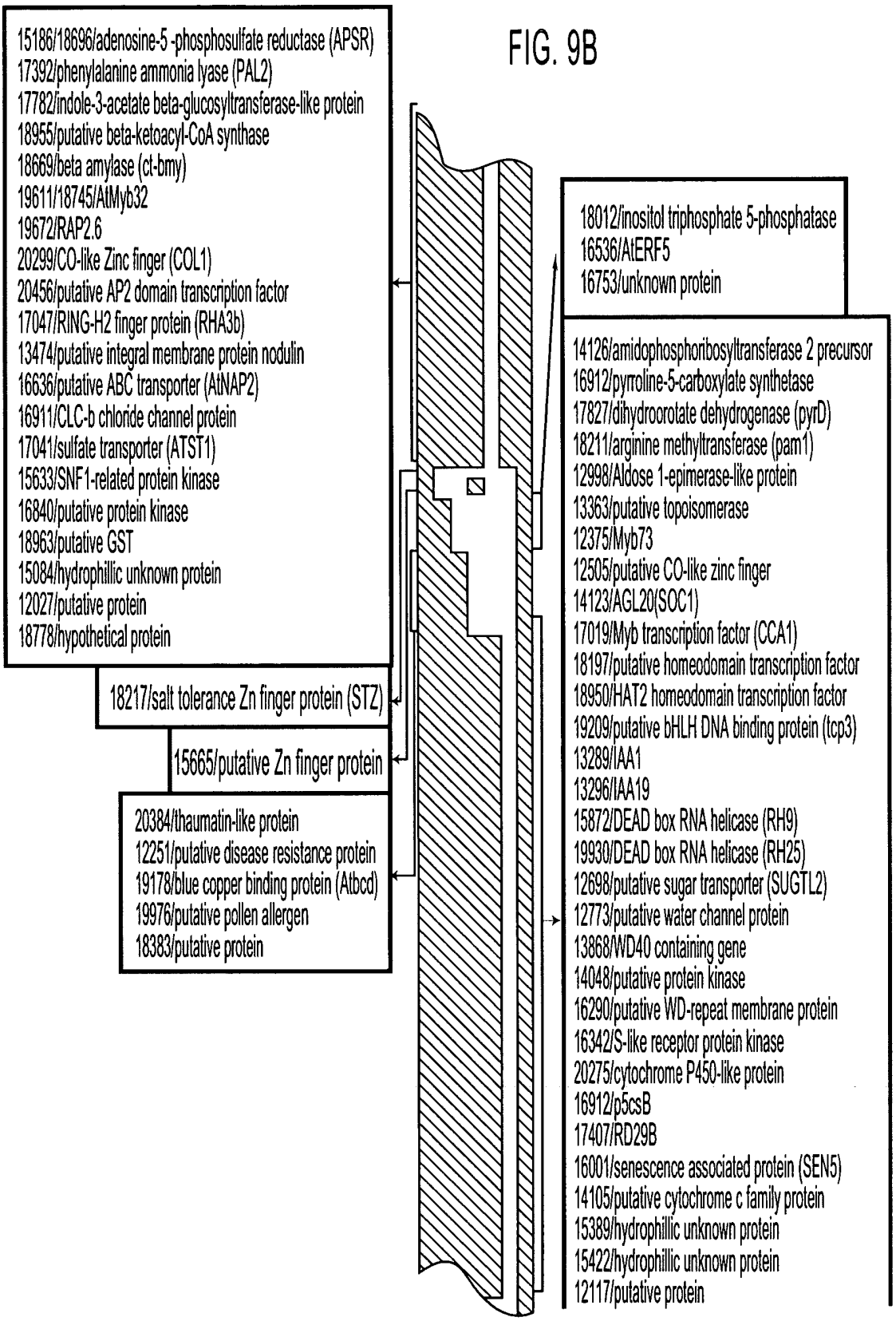

15186/18696/adenosine-5 -phosphosulfate reductase (APSR)
17392/phenylalanine ammonia lyase (PAL2)
17782/indole-3-acetate beta-glucosyltransferase-like protein
18955/putative beta-ketoacyl-CoA synthase
18669/beta amylase (ct-bmy)
19611/18745/AtMyb32
19672/RAP2.6
20299/CO-like Zinc finger (COL1)
20456/putative AP2 domain transcription factor
17047/RING-H2 finger protein (RHA3b)
13474/putative integral membrane protein nodulin
16636/putative ABC transporter (AtNAP2)
16911/CLC-b chloride channel protein
17041/sulfate transporter (ATST1)
15633/SNF1-related protein kinase
16840/putative protein kinase
18963/putative GST
15084/hydrophillic unknown protein
12027/putative protein
18778/hypothetical protein
18217/salt tolerance Zn finger protein (STZ)
15665/putative Zn finger protein
20384/thaumatin-like protein
12251/putative disease resistance protein
19178/blue copper binding protein (Atbcd)
19976/putative pollen allergen
18383/putative protein
18012/inositol triphosphate 5-phosphatase
16536/AtERF5
16753/unknown protein
14126/amidophosphoribosyltransferase 2 precursor
16912/pyrroline-5-carboxylate synthetase
17827/dihydroorotate dehydrogenase (pyrD)
18211/arginine methyltransferase (pam1)
12998/Aldose 1-epimerase-like protein
13363/putative topoisomerase
12375/Myb73
12505/putative CO-like zinc finger
14123/AGL20(SOC1)
17019/Myb transcription factor (CCA1)
18197/putative homeodomain transcription factor
18950/HAT2 homeodomain transcription factor
19209/putative bHLH DNA binding protein (tcp3)
13289/IAA1
13296/IAA19
15872/DEAD box RNA helicase (RH9)
19930/DEAD box RNA helicase (RH25)
12698/putative sugar transporter (SUGTL2)
12773/putative water channel protein
13868/WD40 containing gene
14048/putative protein kinase
16290/putative WD-repeat membrane protein
16342/S-like receptor protein kinase
20275/cytochrome P450-like protein
16912/p5csB
17407/RD29B
16001/senescence associated protein (SEN5)
14105/putative cytochrome c family protein
15389/hydrophillic unknown protein
15422/hydrophillic unknown protein
12117/putative protein

FIG. 9C

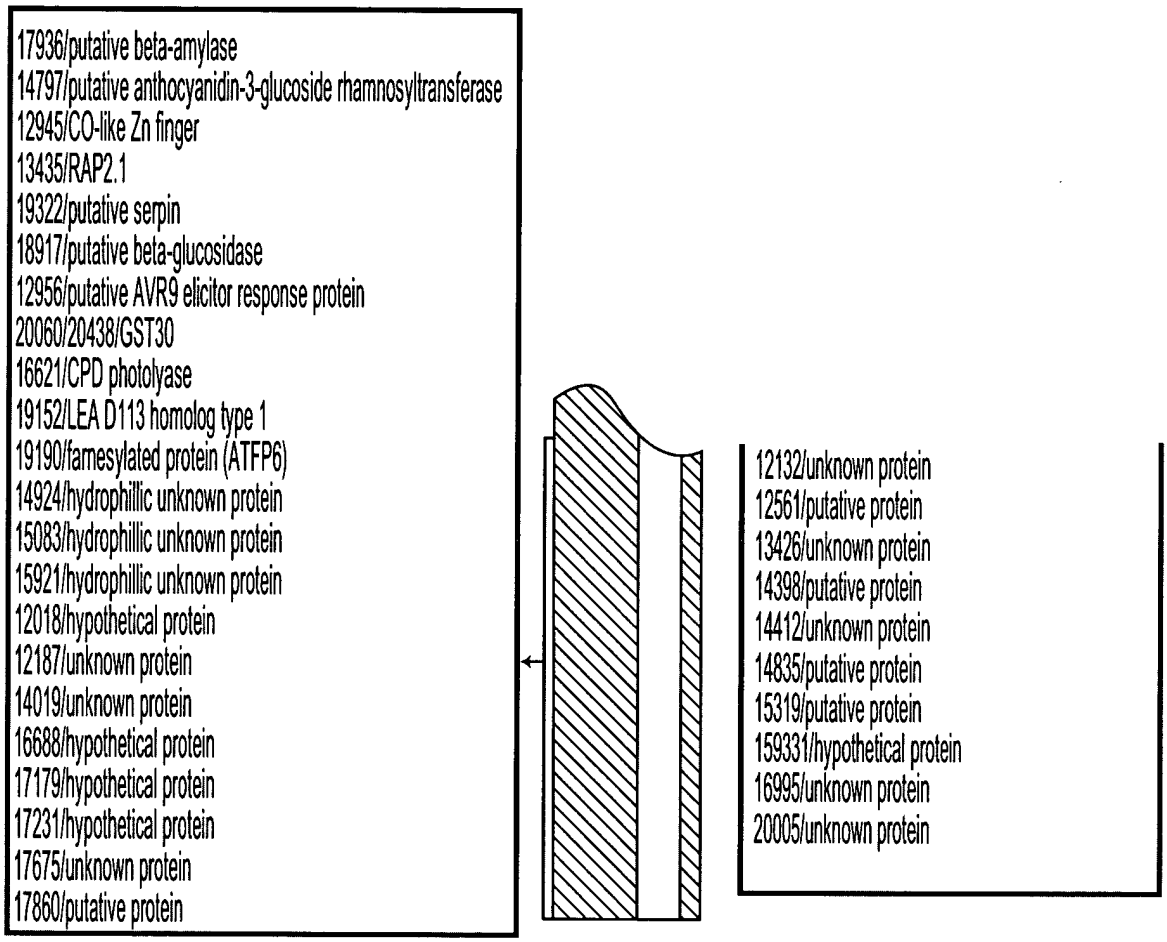

17936/putative beta-amylase
14797/putative anthocyanidin-3-glucoside rhamnosyltransferase
12945/CO-like Zn finger
13435/RAP2.1
19322/putative serpin
18917/putative beta-glucosidase
12956/putative AVR9 elicitor response protein
20060/20438/GST30
16621/CPD photolyase
19152/LEA D113 homolog type 1
19190/farnesylated protein (ATFP6)
14924/hydrophillic unknown protein
15083/hydrophillic unknown protein
15921/hydrophillic unknown protein
12018/hypothetical protein
12187/unknown protein
14019/unknown protein
16688/hypothetical protein
17179/hypothetical protein
17231/hypothetical protein
17675/unknown protein
17860/putative protein
12132/unknown protein
12561/putative protein
13426/unknown protein
14398/putative protein
14412/unknown protein
14835/putative protein
15319/putative protein
159331/hypothetical protein
16995/unknown protein
20005/unknown protein

FIG. 10A

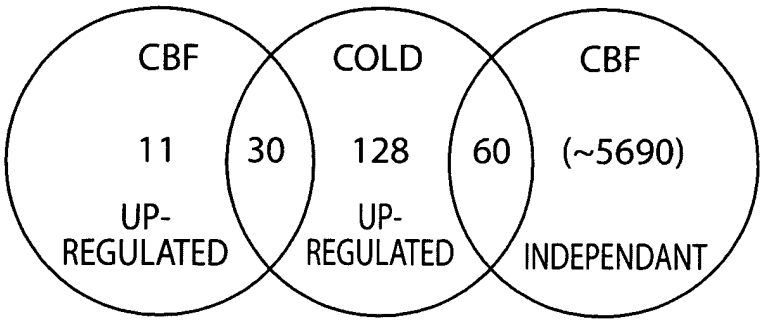


FIG. 10B

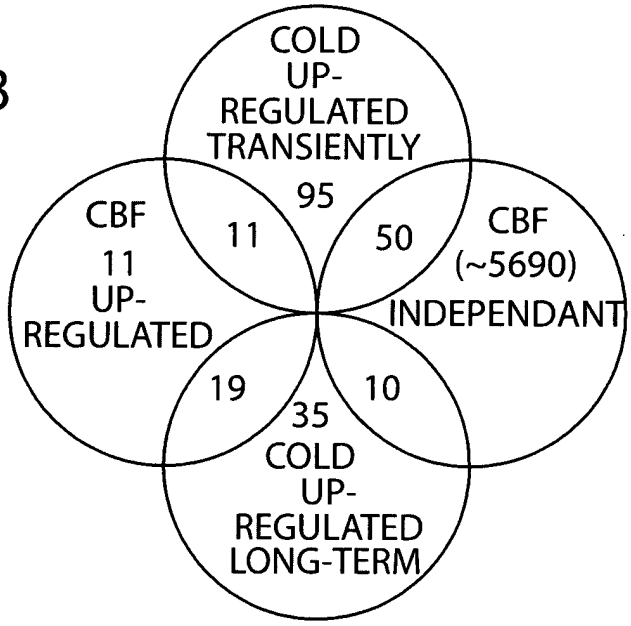


FIG. 10C

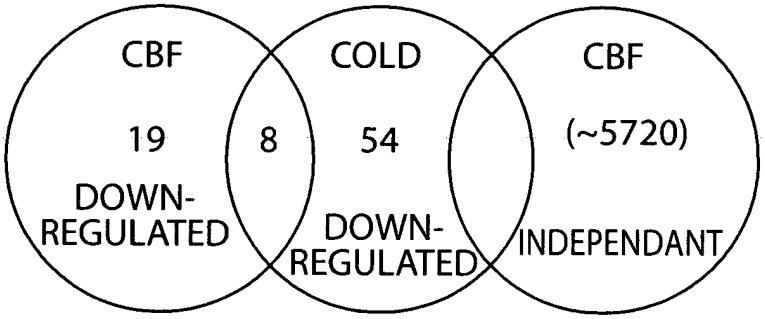


FIG. 11

```
GTATACATAT ACACAACATA ATTCACAACA CAACACAAAC ACATTTCTGT TTTCTCCATT 60
GTTTCAAACC ATAAAAAAAA ACACAGATTA AATGGAATCG AGTAGCGTTG ATGAGAGTAC 120
TACAAGTACA GGTTCCATCT GTGAAACCCC GGCGATAACT CCGGCGAAAA AGTCGTCGGT 180
AGGTAACTTA TACAGGATGG GAAGCGGATC AAGCGTTGTG TTAGATTCAG AGAACGGCGT 240
AGAAGCTGAA TCTAGGAAGC TTCCGTCGTC AAAATACAAA GGTGTGGTGC CACAACCAAA 300
CGGAAGATGG GGAGCTCAGA TTTACGAGAA ACACCAGCGC GTGTGGCTCG GGACATTCAA 360
CGAAGAAGAC GAAGCCGCTC GTGCCTACGA CGTCGCGGTT CACAGGTTCC GTCGCCGTGA 420
CGCCGTCACA AATTTCAAAG ACGTGAAGAT GGACGAAGAC GAGGTCGATT TCTTGAATTC 480
TCATTCGAAA TCTGAGATCG TTGATATGTT GAGGAAACAT ACTTATAACG AAGAGTTAGA 540
GCAGAGTAAA CGGCGTCGTA ATGGTAACGG AAACATGACT AGGACGTTGT TAACGTCGGG 600
GTTGAGTAAT GATGGTGTTT CTACGACGGG GTTTAGATCG GCGGAGGCAC TGTTTGAGAA 660
AGCGGTAACG CCAAGCGACG TTGGGAAGCT AAACCGTTTG GTTATACCGA AACATCACGC 720
AGAGAAACAT TTTCCGTTAC CGTCAAGTAA CGTTTCCGTG AAAGGAGTGT TGTTGAACTT 780
TGAGGACGTT AACGGGAAAG TGTGGAGGTT CCGTTACTCG TATTGGAACA GTAGTCAGAG 840
TTATGTTTTG ACTAAAGGTT GGAGCAGGTT CGTTAAGGAG AAGAATCTAC GTGCTGGTGA 900
CGTGGTTAGT TTCAGTAGAT CTAACGGTCA GGATCAACAG TTGTACATTG GGTGGAAGTC 960
GAGATCCGGG TCAGATTTAG ATGCGGGTCG GGTTTTGAGA TTGTTCGGAG TTAACATTTC 1020
ACCGGAGAGT TCAAGAAACG ACGTCGTAGG AAACAAAAGA GTGAACGATA CTGAGATGTT 1080
ATCGTTGGTG TGTAGCAAGA AGCAACGCAT CTTTCACGCC TCGTAACAAC TCTTCTTCTT 1140
TTTTTTTCT TTTGTTGTTT TAATAATTTT TAAAAACTCC ATTTTCGTTT TCTTTATTTG 1200
CATCGGTTTC TTTCTTCTTG TTTACCAAAG GTTCATGAGT TGTTTTTGTT GTATTGATGA 1260
ACTGTAAATT TTATTTATAG GATAAATTTT AAAAAGGGTT ACTTAGAT 1308
```

FIG. 12

```
ATCATCACAA CTACTATCAC ACCAAACTCA AAAAACACAA ACCACAAGAG GATCATTTCA   60
TTTTTTATTG TTTCGTTTTA ATCATCATCA TCAGAAGAAA AATGGTTGCG ATATCGGAGA  120
TCAAGTCGAC GGTGGATGTC ACGGCGGCGA ATTGTTTGAT GCTTTTATCT AGAGTTGGAC  180
AAGAAAACGT TGACGGTGGC GATCAAAAAC GCGTTTTCAC ATGTAAAACG TGTTTGAAGC  240
AGTTTCATTC GTTCCAAGCC TTAGGAGGTC ACCGTGCGAG TCACAAGAAG CCTAACAACG  300
ACGCTTTGTC GTCTGGATTG ATGAAGAAGG TGAAAACCGTC GTCGCATCCT TGTCCCATAT  360
GTGGAGTGGA GTTTCCGATG GGACAAGCTT TGGGAGGACA CATGAGGAGA CACAGGAACG  420
AGAGTGGGGC TGCTGGTGGC GCGTTGGTTA CACGCGCTTT GTTGCCGGAG CCCACGGTGA  480
CTACGTTGAA GAAATCTAGC AGTGGGAAGA GAGTGGCTTG TTTGGATCTG AGTCTAGGGA  540
TGGTGGACAA TTTGAATCTC AAGTTGGAGC TTGGAAGAAC AGTTTATTGA TTTTATTTAT  600
TTTCCTTAAA TTTTCTGAAT ATATTTGTTT CTCTCATTCT TTGAATTTTT CTTAATATTC  660
TAGATTATAC ATACATCCGC AGATTTAGGA AACTTTCATA GAGTGTAATC TTTTCTTTCT  720
GTAAAAATAT ATTTTACTTG TAGCATTGGA GATTTGTTAT GAGATTATCT TACTTAGCAT  780
TTAGTGAATA ATCTATTTAGC CTATTTTGCC GACGTG                           816
```